

From January 2016 to January 2018, 14 cases of listeriosis in Finland were caused by *L. monocytogenes* sequence type (ST) 6. Therefore, Finland launched in November 2017 an international urgent inquiry (UI) using the Epidemic Intelligence Information System (EPIS) to investigate the presence of this strain in other European Member States.

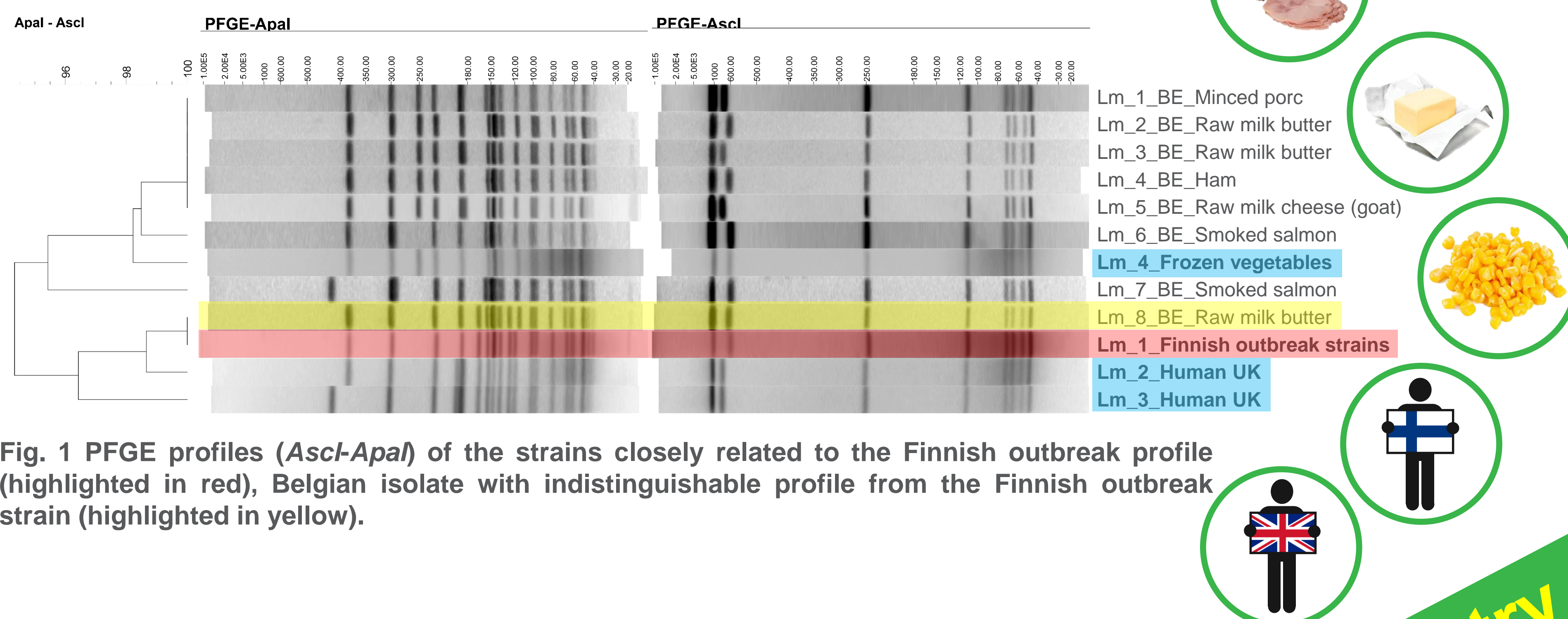


Fig. 1 PFGE profiles (Ascl-Apal) of the strains closely related to the Finnish outbreak profile (highlighted in red), Belgian isolate with indistinguishable profile from the Finnish outbreak strain (highlighted in yellow).

Using the Belgian molecular database, one *L. monocytogenes* IVb strain was found isolated in 2016 from raw milk butter with a Pulsed Field Gel Electrophoresis (PFGE) profile indistinguishable from the Finnish outbreak strain (fig. 1).

The United Kingdom reported two cases of listeriosis caused by *L. monocytogenes* ST6. However, the PFGE profiles of these strains were not identical to the Finnish outbreak strain. Moreover, a number of non-human *L. monocytogenes* ST6 isolates from frozen vegetables, such as corn, were reported with a different PFGE profile.

Solely based on PFGE-analyses the Belgian isolate from raw milk butter belongs to the international outbreak cluster.



The use of the Belgian molecular database and WGS-analyses in a multi-country outbreak investigation of *Listeria monocytogenes* ST6

B. Verhaegen¹ • W. Mattheus² • S. Denayer¹ • S.C.J. De Keersmaecker³ • N.H. Roosens³ • K. Vanneste³ • M. Polet¹ • N. Botteldoorn¹

Scientific Service of Foodborne Pathogens¹, Human Bacterial Diseases² and Transversal & Applied Genomics³, Sciensano, Belgium

Whole Genome Analyses (WGS)-analyses showed that the Belgian isolate from raw milk butter possesses 22 core-genome multi-locus sequence type (cgMLST) allelic differences from the Finnish outbreak strain. As the European outbreak case definition is set at ≤ 7 cgMLST allelic differences this Belgian isolate can be excluded from the international outbreak cluster. Whereas both listeriosis cases reported by the UK and the non-human isolates from frozen vegetables did belong to the outbreak cluster based on WGS-analyses. Corn was identified as a common food item in these non-human isolates. A trace-back investigation identified a Hungarian company that either directly or indirectly delivered corn to companies in all implicated countries, including Belgium.

“Lessons learned”

PFGE clearly lacks the discriminatory capacity and phylogenetic basis of the sequencing-based subtyping methods. Thus its conclusions may be misleading as shown in the present case. Moreover the incongruence between the human surveillance system for *L. monocytogenes* based on WGS and the non-human system based on PFGE will continue to be a major bottleneck in any future foodborne outbreak investigation. Therefore, the implementation of WGS for routine preventive *L. monocytogenes* surveillance for both human and non-human isolates should be considered.

ACKNOWLEDGEMENTS

The authors and members of the NRL Foodborne Outbreaks wishes to thank, the Federal Agency for the Safety of the Food Chain (FASFC) for the excellent collaboration.

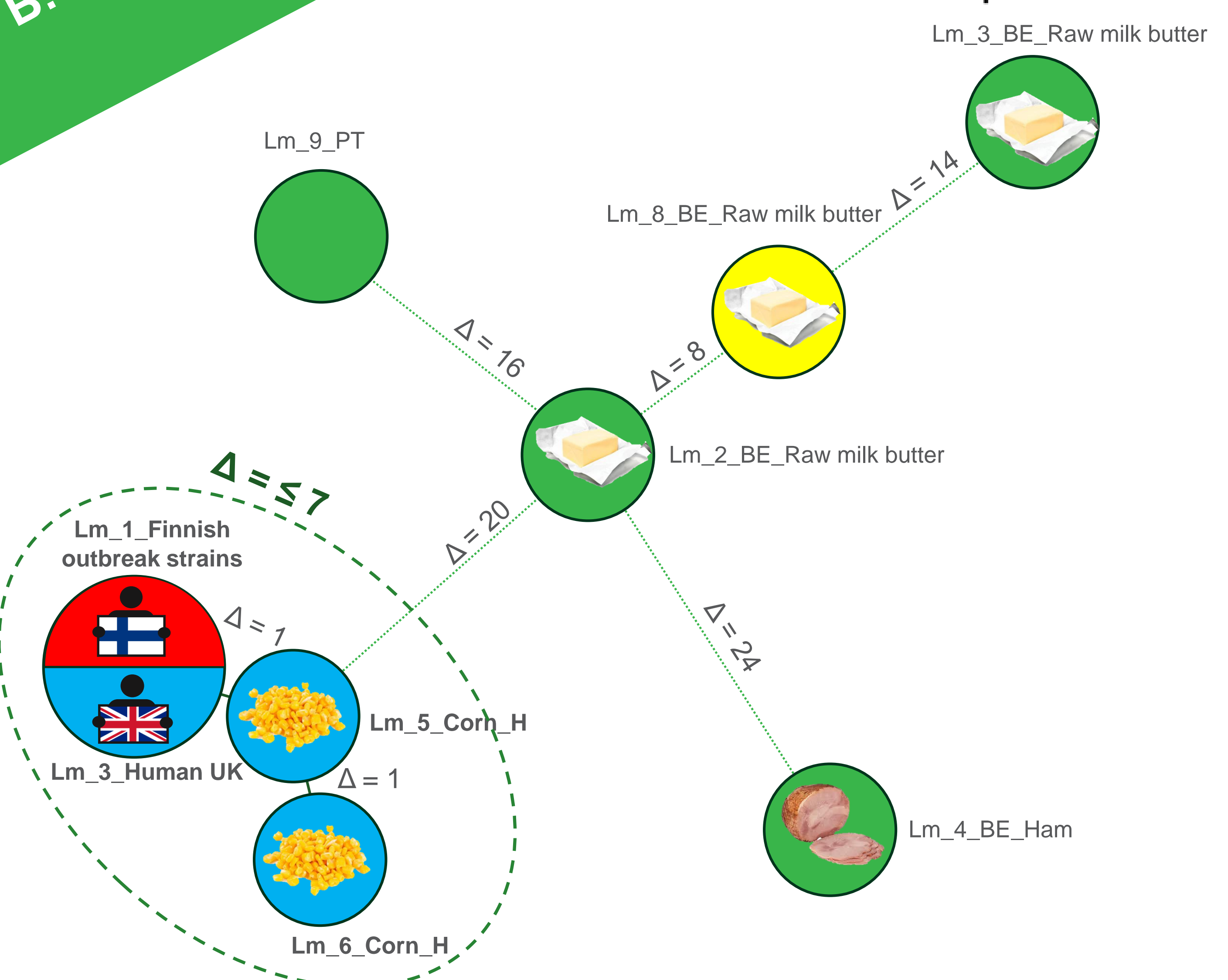


Fig. 2 Minimum Spanning Tree based on the cgMLST of the strains closely related to the Finnish outbreak strain (red node), Belgian isolate with indistinguishable PFGE-profile from the Finnish outbreak strain (yellow node), the number of allelic differences is indicated by Δ ,